

SEQUENCE LISTING

<110> Skeiky, Yasir
Reed, Steven
Alderson, Mark
Corixa Corporation

<120> Fusion Proteins of Mycobacterium Tuberculosis

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<141> 2000-06-20

<150> US 09/056,556
<151> 1998-04-07

<150> US 09/223,040
<151> 1998-12-30

<150> WO PCT/US99/07717
<151> 1999-04-07

<150> US 09/287,849
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<150> US 60/158,338
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<170> PatentIn Ver. 2.1

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<223> Ra35

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<213> Mycobacterium tuberculosis
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35 40 45
Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
50 55 60
Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
65 70 75 80
Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
85 90 95
Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
100 105 110
Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
115 120 125
Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
130 135 140
Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
145 150 155 160
Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
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<213> Mycobacterium tuberculosis

<220>
<223> MTB32A (TbRa35FL) cDNA

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 <213> Mycobacterium tuberculosis

<220>
 <223> MTB32A (TbRa35FL) protein

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 35 40 45
 Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Ala Pro Gln Val Val
 50 55 60
 Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
 65 70 75 80
 Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
 85 90 95
 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
 100 105 110
 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
 115 120 125
 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
 130 135 140
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 180 185 190
 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
 195 200 205
 Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
 210 215 220
 Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala
 225 230 235 240
 Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly
 245 250 255
 Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu
 260 265 270

Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val
275 280 285
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Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp
305 310 315 320
Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp Gln
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<220>
<223> MTBRa12 C-terminus of MTB32A (Ra35FL)

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<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> MTBRa12 C-terminus of MTB32A (Ra35FL)

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Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
35 40 45
Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
50 55 60
Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
65 70 75 80
Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
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Gly Pro Pro Ala
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 Gln Asn Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met
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 225 230 235 240
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 260 265 270
 Ala Ala Ala Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala
 275 280 285
 Met Ser Ser Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly
 290 295 300
 Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val
 305 310 315 320
 Pro Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg
 325 330 335
 Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly
 340 345 350
 Gln Met Leu Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly
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<222> (1)..(1791)
<223> MTB59F

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<212> PRT
<213> Artificial Sequence
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     20          25          30
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 85 90 95
 Ala Gln Val Arg Val Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu
 100 105 110
 Thr Val Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile
 115 120 125
 Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val
 130 135 140
 Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met
 145 150 155 160
 Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Leu Leu Pro
 165 170 175
 Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln
 180 185 190
 Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Asn Gln Leu
 195 200 205
 Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu Ala Gln Pro Thr Gln
 210 215 220
 Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser
 225 230 235 240
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 245 250 255
 Met Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser
 260 265 270
 Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Gln Ala Val Gln Thr
 275 280 285
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 305 310 315 320
 Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala Trp Ala Ala Asn
 325 330 335
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 340 345 350
 Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu Gly Gly Leu Pro Val
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 Gly Gln Met Gly Ala Arg Ala Gly Gly Leu Ser Gly Val Leu Arg
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 420 425 430
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 450 455 460
 Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly
 465 470 475 480
 Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val
 485 490 495
 Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile
 500 505 510
 Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser
 515 520 525

Gly Gly Gln Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala
 530 535 540
 Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu
 545 550 555 560
 Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp
 565 570 575
 Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn
 580 585 590
 Thr Ala Ala Ser
 595

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<210> 11
<211> 2287
<212> DNA
<213> Mycobacterium tuberculosis

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:fusion
      protein Ra12-TbH9-Ra35 (MTB72F)

<220>
<221> modified_base
<222> (30)
<223> n = g, a, c or t

<220>
<221> modified_base
<222> (33)
<223> n = g, a, c or t

<220>
<221> CDS
<222> (42)..(2231)
<223> MTB72F

<220>
<221> modified_base
<222> (2270)
<223> n = g, a, c or t

<400> 11
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acacggccgc gtccgataac ttccagctgt cccagggtgg gcagggattc gccattccga 120
tcgggcagggc gatggcgatc gcggggccaga tccgatcggg tgggggtca cccaccgttc 180
atatcgccgc taccgccttc ctccgcttgg gtgttgcga caacaacggc aacggcgac 240
gagtccaaacg cgtggtcggg agcgctccgg cggcaagtct cggcatctcc accggcgacg 300
tgatcaccgc ggtcgacggc gctccgatca actcggccac cgcgatggcg gacgcgccta 360
acgggcatac tcccgggtgac gtcatctcgg tgacctggca aaccaagtct ggcggcacgc 420
gtacagggaa cgtgacattg gccgaggggac ccccgccga attcatgtt gatttcgggg 480
cggttaccacc ggagatcaac tccgcgagga tgtacggccgg cccgggttcg gcctcgctgg 540
tggccgcggc tcagatgtgg gacagcggtt cgagtgcacgt gtttccggcc gcgtcgccgt 600
ttcagtcgggt ggtctgggt ctgacgggtt ggtcgtggat aggttgcgt gcggtctga 660
tggtggccggc ggcctcgccg tatgtggcgt ggatgagcgt caccgcgggg caggccgagc 720
tgaccgcgcg ccagggtccgg gttgcgtccgg cggcctacga gacggcgat gggctgacgg 780
tgccccgcgc ggtgatcgcc gagaaccgtt ctgaactgtat gattctgata gcgaccaacc 840
tcttggggca aaacaccccg gcgatcgccg tcaacgaggc cgaataacggc gagatgtggg 900
cccaagacgc cgccgcgtt tttggctacg ccgcggccac ggcgacggcg acggcgacgt 960
tgctgccgtt cgaggaggcg ccggagatga ccagcgccgg tggctccctc gagcaggccg 1020
  
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ccgcggtcga ggaggcctcc gacaccgccc cggcgaacca gttgatgaac aatgtcccc 1080
 aggcgctgca acagctggcc cagcccacgc agggcaccac gccttcttcc aagctgggtg 1140
 gcctgtggaa gacggtctcg ccgcacatcggt cgccgatcag caacatggtg tcgatggcca 1200
 acaaccacat gtcgatgacc aactcgggtg tgtcgatgac caaacacctg agctcgatgt 1260
 tgaagggctt tgctccggcg gcgcccccc agggcgtgca aaccgcggcg caaaacgggg 1320
 tccggcgat gagctcgctg ggcagctcg tgggttctt gggctggc ggtgggtgg 1380
 ccgccaactt gggtcggcg gcctcggtcg gttcggtgtc ggtgcccgag gcctggccg 1440
 cggccaacca ggcagtccacc cggcggcgcc gggcgctgcc gctgaccagc ctgaccagcg 1500
 ccgcggaaag agggcccccgg cagatgctgg gcgggctgcc ggtggggcag atgggcgcca 1560
 gggccgggtgg tgggtcagt ggtgtgtcg gtgttccggcc ggcacccat gtgatgccc 1620
 attctccggc agccggcgat atcgcggccgc cggccttgcgc gcaggaccgg ttgcggact 1680
 tcccccgct gcccctcgac ccgtccgaga tggtcggcca agtggggcca caggtggtca 1740
 acatcaacac caaactgggc tacaacaacg ccgtggcgcc cgggaccggc atcgtcatcg 1800
 atcccaacgg tgcgtgtcg accaacaacc acgtgatecg gggcgccacc gacatcaatg 1860
 cgttcagcgt cggctccggc caaacctacg gcgtcgatgt ggtcggttat gaccgcaccc 1920
 agatgtcgc ggtgtcgag ctgcgcggtg ccggtggcct gccgtcgcc gegatcggtg 1980
 gccgcgtcgc ggttggtgag cccgtcgctg cgatggcaa cagcggtgg cagggcggaa 2040
 cggcccggtgc ggtgcctggc agggtggtcg cgctcgccca aaccgtgcag ggtcggtt 2100
 cgctgaccgg tgccgaagag acattgaacg ggttgcataa gttcgatgcc gogatccagc 2160
 ccggtgattc gggcgggccc gtcgtcaacg gcctaggaca ggtggtcggt atgaacacgg 2220
 ccgcgtccta ggatatccat cacactggcg gcccgtcgag cagatccgn tgtaacaaag 2280
 cccgaaaa 2287

<210> 12
 <211> 729
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence:fusion
 protein Ra12-TbH9-Ra35 (MTB72F)

<400> 12
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 1 5 10 15
 Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
 20 25 30
 Ile Ala Gly Gln Ile Arg Ser Gly Gly Ser Pro Thr Val His Ile
 35 40 45
 Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn
 50 55 60
 Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu
 65 70 75 80
 Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile
 85 90 95
 Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly
 100 105 110
 Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr
 115 120 125
 Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Met Val Asp
 130 135 140
 Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly
 145 150 155 160
 Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val
 165 170 175
 Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp
 180 185 190
 Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val
 195 200 205
 Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln
 210 215 220

Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala Ala Tyr Glu
 225 230 235 240
 Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg
 245 250 255
 Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr
 260 265 270
 Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln
 275 280 285
 Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr
 290 295 300
 Ala Thr Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly
 305 310 315 320
 Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala
 325 330 335
 Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu
 340 345 350
 Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu
 355 360 365
 Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn Met Val Ser
 370 375 380
 Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val Ser Met Thr
 385 390 395 400
 Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Arg
 405 410 415
 Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser
 420 425 430
 Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Val Ala Ala
 435 440 445
 Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala
 450 455 460
 Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro
 465 470 475 480
 Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu
 485 490 495
 Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly Gly Leu
 500 505 510
 Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His Ser
 515 520 525
 Pro Ala Ala Gly Asp Ile Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe
 530 535 540
 Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val Ala Gln
 545 550 555 560
 Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn
 565 570 575
 Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val
 580 585 590
 Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe
 595 600 605
 Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp
 610 615 620
 Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu
 625 630 635 640
 Pro Ser Ala Ala Ile Gly Gly Val Ala Val Gly Glu Pro Val Val
 645 650 655
 Ala Met Gly Asn Ser Gly Gly Gln Gly Gly Thr Pro Arg Ala Val Pro
 660 665 670
 Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu
 675 680 685
 Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala
 690 695 700

Ile Gln Pro Gly Asp Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln
705 710 715 720
Val Val Gly Met Asn Thr Ala Ala Ser
725

<210> 13
<211> 500
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> Mtb8.4 (DPV)

<400> 13
cgtggcaatg tcgttgaccg tcggggccgg ggtcgcctcc gcagatcccg tggacgcgg 60
cattaacacc actgtcaatt acgggcagg agtagctgcg ctcaacgcga cggatccggg 120
ggctgcccga cagttcaacg cctcaccggg ggccgcagtc tatggcgcga atttgcgc 180
cgcacccgcca cctcagcgcg ctgcgcattc cgcccaattt caagctgtgc cgggggcggc 240
acagtacatc ggcctgtcg agtcgggtgc cggccctgc aacaactatt aagcccatgc 300
gggccccatc ccgcgaccgg gcacatgtgc cggggctagg ccagattgcc ccgcgcctca 360
acggggccga tcccgcgacc cggcatgtc gccccggcta ggccagattt ccccgctct 420
caacggggccg catctcggtc cgaatttcgtc cagccccggg gatccactag ttcttagagcg 480
gccggccaccg cgggtggact 500

<210> 14
<211> 96
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> Mtb8.4 (DPV)

<400> 14
Val Ala Met Ser Leu Thr Val Gly Ala Gly Val Ala Ser Ala Asp Pro
1 5 10 15
Val Asp Ala Val Ile Asn Thr Thr Cys Asn Tyr Gly Gln Val Val Ala
20 25 30
Ala Leu Asn Ala Thr Asp Pro Gly Ala Ala Gln Phe Asn Ala Ser
35 40 45
Pro Val Ala Gln Ser Tyr Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro
50 55 60
Gln Arg Ala Ala Met Ala Ala Gln Leu Gln Ala Val Pro Gly Ala Ala
65 70 75 80
Gln Tyr Ile Gly Leu Val Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr
85 90 95

<210> 15
<211> 585
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> Mtb9.8 (MSL)

<400> 15
tggattccga tagcggttgc ggccctcga cggcgacca cggcgccgag gcctccgaac 60
ggggggccgg gacgcgtggaa ttccgcggaa ccgcacccaa agaacgcgg gtccggccgg 120
tcgggctgac cgcactggcc ggtgatgagt tcggcaacgg ccccccggatg ccgcgtgtgc 180

cggggacctg ggagcaggc agcaacgagc ccgaggcgcc cgacggatcg gggagagggg 240
gaggcgacgg cttaccgcac gacagcaagt aaccgaattc cgaatcacgt ggaccgtac 300
gggtcgaaag gagagatgtt atgagcctt tggatgctca tatcccacag ttggtggcct 360
cccagtccgc gttgccgccc aaggcggggc tgatgcggca cacgatcggt caggccgagc 420
aggcggcgat gtcggcttag gcgttccacc agggggagtc gtcggccgcg tttcaggccg 480
cccatgcccc gtttgtggcg gccggccgcca aagtcaacac cttgtggat gtcgcgcagg 540
cgaatctggg tgaggccgccc ggtacctatg tggccgcccga tgctg 585

<210> 16
<211> 97
<212> PRT
<213> *Mycobacterium tuberculosis*

<220>
<223> Mtb9.8 (MSL)

<400> 16
Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser
1 5 10 15
Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala
20 25 30
Glu Gln Ala Ala Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser
35 40 45
Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Lys
50 55 60
Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala
65 70 75 80
Gly Thr Tyr Val Ala Ala Asp Ala Ala Ala Ser Thr Tyr Thr Gly
85 90 95
Phe

<210> 17
<211> 1742
<212> DNA
<213> *Mycobacterium tuberculosis*

<220>
<223> Mtb9.9A (MTI, MTI-A)

<220>
<221> modified_base
<222> (1)..(1742)
<223> n = g, a, c or t

<400> 17
ccgctctctt tcaacgtcat aagttcggtg ggcagtcgg ccgcgcgtgc atatggcacc 60
aataacgcgt gtcccatgga taccggacc gcacgacggt agagcgatc agcgcagccg 120
gtgccgaaca ctaccgcgtc cacgctcagc cctgcccgt tgccgaagat cgagccagg 180
ttctcatgtt cgtaaacgccc ttccaaact ggcacgggtgc ggcgcggc gaccaccta 240
gcaacgctcg gtcggccac ccggcgccg gctgccaaca ccccacgatt gagatggaag 300
ccgatcaccc gtgccatgac atcagccgac gctcgatagt acggcgccgac gacaccggcc 360
agatcatcct tgagctcgcc cagccggcgg tcgtgcccga acagcgcac cggcgtgaac 420
cgtgaggcca gcatgcgtc caccaccagc acaccctcggt cgatcacaa cgccttgcgg 480
gtcggcagat cgggacnacl gtcgatgtt ttcaggtcac gaaatcgatc gagccgtggg 540
tcgtcggtt cgcagacgtc ctgaacatcg aggccgtcg ggtgctggc acaacggcc 600
tcggtcacgg gcttcgtcg accagagcca gcatcagatc ggcggcgctg cgcaggatgt 660
cacgctcgat gcggttcagc gtcgcgagcc gctcagccag ccactttgc agagagccgt 720
tgctggatt aattggaga ggaagacagc atgtcgatcg tgaccacaca gccggaagcc 780
ctggcagctg cggcgccaa cctacagggat attggcacga caatgaacgc ccagaacgc 840

gccgcggctg ctccaaccac cggagtagtg cccgcagccg ccgatgaagt atcagcgctg 900
 accgcggctc agtttgcgtc gcacgcgcag atgtaccaaa cggtcagcgc ccaggccgcg 960
 gccattcact aaatgttcgt gaacacgctg gtggccagtt ctggctata cgccggccacc 1020
 gagggcggcca acgcagccgc tgccggctga acgggctcgc acgaacctgc tgaaggagag 1080
 ggggaacatc cggagttctc gggtcaggggg ttgcgccagc gcccagccga ttcaagntatc 1140
 ggcgtcata acagcagacg atctaggcat tcagtaactaa ggagacaggc aacatggcct 1200
 cacgttttat gacggatccg catgcgtatgc gggacatggc gggccgttt gaggtgcacg 1260
 cccagacggt ggaggacgag gctgcggga tggggcgtc cgccaaaac atttccgggt 1320
 cgggctggag tggcatggcc gaggcgacac cgctagacac catgacactag atgaatcagg 1380
 cgttgccaa catcgtaac atgcgtcaca ggggtgcgtga cgggctgggt cggcacgcca 1440
 acaantacga acagcaagag caggcctccc agcagatcct gagcagtag cgccgaaagc 1500
 cacagctngn tacgnnttct cacattagga gaacaccaat atgacgatttta attaccagtt 1560
 cggggacggtc gacgctcatg ggcctatgt ccgcgtctag gccgcgtcgc ttgaggcgga 1620
 gcatcaggcc atcggtcgat atgtgttggc cgggggtgac ttttggggcg gcccgggttc 1680
 ggtggcttgc caggagttca ttacccttgtt gggccgttaac ttccagggtga tctacgagca 1740
 gg 1742

<210> 18
 <211> 94
 <212> PRT
 <213> *Mycobacterium tuberculosis*

<220>
 <223> Mtb9.9A (MTI, MTI-A)

<400> 18
 Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met
 1 5 10 15
 Ile Arg Ala Leu Ala Gly Leu Leu Glu Ala Glu His Gln Ala Ile Ile
 20 25 30
 Ser Asp Val Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala Gly Ser Ala
 35 40 45
 Ala Cys Gln Gly Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile
 50 55 60
 Tyr Glu Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn
 65 70 75 80
 Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala
 85 90

<210> 19
 <211> 1200
 <212> DNA
 <213> *Mycobacterium tuberculosis*

<220>
 <223> MTB40 (HTCC#1) cDNA

<400> 19
 caggcatgag cagagcggttc atcatcgatc caacgatcag tgccattgac ggcttgcgtac 60
 accttctggg gatttggata cccaaaccaag ggggtatcct ttactcctca ctagagtact 120
 tcgaaaaagc cctggaggag ctggcagcag cgtttccggg tggatggctgg ttaggttcgg 180
 cccggggacaa atacgccccca aaaaaccgca accacgtgaa ttttttccag gaactggcag 240
 acctcgatcg tcagctcatc agcctgatcc acgaccaggc caacgcgtc cagacgaccc 300
 gccgacatcct ggagggcgcc aagaaaggtc tcgagttcgt ggcgcgggtg gctgtggacc 360
 tgacacctat cccggtcgtc gggcacgccc tatcggccgc cttccaggcg ccgttttgcg 420
 cgggcgcgtat ggcgttagtg ggcggcgcgc ttgcctactt ggtcgtgaaa acgctgatca 480
 acgcgactca actcctcaaa ttgcgttgcga aattggcgga gttggcgtcg gcccgcattg 540
 cggacatcat ttgcgtatgtc gcccgcgtca tcaaggccac cctcgagaa gtgtgggagt 600
 tcatacacaat cgcgtcaac ggcctgaaag agctttggga caagctcagc ggggtgggtga 660

ccggactgtt ctctcgaggg tggtcgaacc tggagtccctt ctttgcgggc gtccccggct 720
tgacccggcgc gaccagggc ttgtcgcaag tgactggctt gttcggtgcg gccggcttgt 780
ccgcacatcgctc gggcttggct cacgcggata gcctggcgag ctcagccagc ttgcccggcc 840
tggccggcat tggggggggg tccgggtttg gggcttgcc gagcctggct caggtccatg 900
ccgcctcaac tcggcaggcg ctacggcccc gagctgatgg cccggtcgcc gcccgtgccg 960
agcaggtcgg cggcagtcg cagctggct cgcgcaggg ttcccaaggt atgggcggac 1020
ccgtaggcat gggcggcatg caccctctt cggggcgctc gaaaggagacg acgacgaaga 1080
agtactcgga aggccgcggcg gcgggcactg aagacgccga ggcgcgcaca gtcgaagctg 1140
acgcggcgg tggcaaaaag gtgctggtaa gaaacgtcgt ctaacggcat ggcgagccaa 1200

<210> 20
<211> 392
<212> PRT
<213> *Mycobacterium tuberculosis*

<220>
<223> MTB40 (HTCC#1)

<400> 20
Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala Ile Asp Gly
1 5 10 15
Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu
20 25 30
Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala
35 40 45
Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
50 55 60
Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu
65 70 75 80
Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln
85 90 95
Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu Glu Phe Val
100 105 110
Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val Gly His Ala
115 120 125
Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala Met Ala Val
130 135 140
Val Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn Ala
145 150 155 160
Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala
165 170 175
Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Thr
180 185 190
Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
195 200 205
Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
210 215 220
Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
225 230 235 240
Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
245 250 255
Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
260 265 270
Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Ser Gly Phe
275 280 285
Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln
290 295 300
Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln
305 310 315 320

Val	Gly	Gly	Gln	Ser	Gln	Leu	Val	Ser	Ala	Gln	Gly	Ser	Gln	Gly	Met
							325								335
Gly	Gly	Pro	Val	Gly	Met	Gly	Gly	Met	His	Pro	Ser	Ser	Gly	Ala	Ser
							340								350
Lys	Gly	Thr	Thr	Thr	Lys	Lys	Tyr	Ser	Glu	Gly	Ala	Ala	Ala	Gly	Thr
							355								365
Glu	Asp	Ala	Glu	Arg	Ala	Pro	Val	Glu	Ala	Asp	Ala	Gly	Gly	Gly	Gln
							370								380
Lys	Val	Leu	Val	Arg	Asn	Val	Val								
							385								390

<210> 21
<211> 1441
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> MTB41 (MTCC#2)

<400> 21

gagggttgctg	gcaatggatt	tcgggctttt	acctccggaa	gtgaattcaa	gccgaatgt	60
ttcccggtccg	gggcgggagt	cgatgcttagc	cgcgcgggccc	gcctgggacg	gtgtggccgc	120
ggagttgact	tccgcccgcgg	tctcgatgg	atcggtggtg	tcgacgctga	tcgttgagcc	180
gtggatgggg	ccggcggcgg	ccgcgatggc	ggccgcggca	acgcccgtatg	tggggtgtggct	240
ggccgcacg	gcggcgctgg	cgaaggagac	ggccacacag	gcgagggcag	cggcggaaagc	300
gtttgggacg	gcgttgcgca	tgacgggtgcc	accatccctc	gtcgcggcca	accgcagccg	360
gttgatgtcg	ctgggtcgccg	cgaacattct	ggggcaaaaac	agtgcggcga	tcgcggctac	420
ccaggccgag	tatgcccggaa	tgtgggcccc	agacgctgcc	gtgatgtaca	gctatgaggg	480
ggcatctcg	gccgcgtcgg	cgttgcgc	gttcaactcca	cccgtgcaag	gcaccggccc	540
ggccgggccc	gcggccgcag	ccgcggcgcac	ccaagccg	ggtgcggg	ccgttgcgg	600
tgcacaggcg	acactggccc	agctgcccc	gggatcctg	agcgcacattc	tgtccgcatt	660
ggccgcacac	gctgatccgc	tgacatcg	actgttgggg	atcgcgtcga	ccctcaaccc	720
gcaagtccg	tccgctcagc	cgatagtgtat	ccccaccccg	ataggggaa	tggacgtat	780
cgcgc	ctac	attgcatcca	tcgcgacccg	cagcattgc	ctcgcgatca	840
cagaccctgg	cacatcg	tatacggaa	cgccggcggg	ctgggaccga	cgcagg	900
tccactgagt	tcggcgaccg	acgagccg	gcccactgg	ggcccttcg	ggggcgcgg	960
gccgggtgtcc	gcgggcgtcg	gccacgc	attagtcg	gcgttgcgg	tgccgcacag	1020
ctggaccacg	ccgcggccgg	agatccag	cgccgttc	gcaacaccca	ccttcagctc	1080
cagcgccggc	ccgcgacccg	cggccctaaa	cggatgccc	gcaggcctgc	tcagcggat	1140
ggctttggcg	agcctggccg	cacgcgg	gacgggcgg	ggcggcaccc	gtagcggc	1200
cagca	ctgac	ggccaagagg	acggccgaa	accccccgt	gttgtgatta	1260
gccggccgg	aaccccccgc	ggtaaaagtc	cgcaaccgt	tcgtcgccgc	gcggaaaatg	1320
cctggtgagc	gtggctatcc	gacgggcgt	tcacaccgt	tgttagtagcg	tacggctatg	1380
gacgacgg	tctggattct	cgccggctat	cagagcgatt	ttgctcgaa	cctcagcaa	1440
						1441
g						

<210> 22
<211> 423
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> MTB41 (MTCC#2)

<400> 22

Met	Asp	Phe	Gly	Leu	Leu	Pro	Pro	Glu	Val	Asn	Ser	Ser	Arg	Met	Tyr
1							5							10	15
Ser	Gly	Pro	Gly	Pro	Glu	Ser	Met	Leu	Ala	Ala	Ala	Ala	Trp	Asp	
							20							25	30

Gly Val Ala Ala Glu Leu Thr Ser Ala Ala Val Ser Tyr Gly Ser Val
 35 40 45
 Val Ser Thr Leu Ile Val Glu Pro Trp Met Gly Pro Ala Ala Ala Ala
 50 55 60
 Met Ala Ala Ala Ala Thr Pro Tyr Val Gly Trp Leu Ala Ala Thr Ala
 65 70 75 80
 Ala Leu Ala Lys Glu Thr Ala Thr Gln Ala Arg Ala Ala Ala Glu Ala
 85 90 95
 Phe Gly Thr Ala Phe Ala Met Thr Val Pro Pro Ser Leu Val Ala Ala
 100 105 110
 Asn Arg Ser Arg Leu Met Ser Leu Val Ala Ala Asn Ile Leu Gly Gln
 115 120 125
 Asn Ser Ala Ala Ile Ala Ala Thr Gln Ala Glu Tyr Ala Glu Met Trp
 130 135 140
 Ala Gln Asp Ala Ala Val Met Tyr Ser Tyr Glu Gly Ala Ser Ala Ala
 145 150 155 160
 Ala Ser Ala Leu Pro Pro Phe Thr Pro Pro Val Gln Gly Thr Gly Pro
 165 170 175
 Ala Gly Pro Ala Ala Ala Ala Ala Thr Gln Ala Ala Gly Ala Gly
 180 185 190
 Ala Val Ala Asp Ala Gln Ala Thr Leu Ala Gln Leu Pro Pro Gly Ile
 195 200 205
 Leu Ser Asp Ile Leu Ser Ala Leu Ala Ala Asn Ala Asp Pro Leu Thr
 210 215 220
 Ser Gly Leu Leu Gly Ile Ala Ser Thr Leu Asn Pro Gln Val Gly Ser
 225 230 235 240
 Ala Gln Pro Ile Val Ile Pro Thr Pro Ile Gly Glu Leu Asp Val Ile
 245 250 255
 Ala Leu Tyr Ile Ala Ser Ile Ala Thr Gly Ser Ile Ala Leu Ala Ile
 260 265 270
 Thr Asn Thr Ala Arg Pro Trp His Ile Gly Leu Tyr Gly Asn Ala Gly
 275 280 285
 Gly Leu Gly Pro Thr Gln Gly His Pro Leu Ser Ser Ala Thr Asp Glu
 290 295 300
 Pro Glu Pro His Trp Gly Pro Phe Gly Gly Ala Ala Pro Val Ser Ala
 305 310 315 320
 Gly Val Gly His Ala Ala Leu Val Gly Ala Leu Ser Val Pro His Ser
 325 330 335
 Trp Thr Thr Ala Ala Pro Glu Ile Gln Leu Ala Val Gln Ala Thr Pro
 340 345 350
 Thr Phe Ser Ser Ala Gly Ala Asp Pro Thr Ala Leu Asn Gly Met
 355 360 365
 Pro Ala Gly Leu Leu Ser Gly Met Ala Leu Ala Ser Leu Ala Ala Arg
 370 375 380
 Gly Thr Thr Gly Gly Gly Thr Arg Ser Gly Thr Ser Thr Asp Gly
 385 390 395 400
 Gln Glu Asp Gly Arg Lys Pro Pro Val Val Val Ile Arg Glu Gln Pro
 405 410 415
 Pro Pro Gly Asn Pro Pro Arg
 420

<210> 23
 <211> 154
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <223> ESAT-6

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<400> 23
atgacagagc agcagtggaa tttcgccgggt atcgaggccg cggcaagcgc aatccaggga 60
aatgtcacgt ccattcattc cctccttgc gaggggaaagc agtccctgac caagctcgca 120
gcggcctggg gcggtagcgg ttcggaagcg tacc 154

<210> 24
<211> 51
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> ESAT-6

<400> 24
Met Thr Glu Gln Gln Trp Asn Phe Ala Gly Ile Glu Ala Ala Ala Ser
1 5 10 15
Ala Ile Gln Gly Asn Val Thr Ser Ile His Ser Leu Leu Asp Glu Gly
20 25 30
Lys Gln Ser Leu Thr Lys Leu Ala Ala Ala Trp Gly Gly Ser Gly Ser
35 40 45
Glu Ala Tyr
50

<210> 25
<211> 851
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> MTB39 (TbH9) cDNA

<400> 25
ctgcagggtg gcgtggatga gcgtcaccgc gggcaggcc gagctgaccg ccgcccaggt 60
ccgggttgct gcggccgcct acgagacggc gtatgggctg acgggtcccc cgccgggtat 120
cggcgagaac cgtgctgaac tgatgattct gatacgacc aacctttgg ggcaaaacac 180
cccgccgatc gcggtaacg aggccgaata cggcgagatg tgggccaag acgcccgcgc 240
gatgtttggc tacggccgcgg cgacggcgcac ggcgacggcg acgttgcgc cgttcgagga 300
ggcgccggag atgaccagcg cgggtggct cctcgagcag gccgcccgg tcgaggaggc 360
ctccgacacc gccgcggcga accagttat gaacaatgtg ccccaggcgc taaaacagtt 420
ggcccagccc acgcaggcga ccacgccttc ttccaagctg ggtggctgt ggaagacggt 480
ctcgccgcat cggtcgccga tcagcaacat ggtgtcgatg gccaacaacc acatgtcgat 540
gaccaactcg ggtgtgtcga tgaccaacac cttagctcg atgttgaagg gctttgcctc 600
ggcgccggcc gcccaggccg tgcaaaccgc ggcgcaaaac ggggtccggg cgatgagctc 660
gctgggcagc tggctgggtt ctgcgggtct gggcggtggg gtggccgcca acttgggtcg 720
ggcggccctcg gtacggatg gtcacccggaa tggcgaaaa tatgcanagt ctggtcggcg 780
gaacggtggt ccggcgtaag gtttaccccc gtttctgga tgcggtaac ttctgtcaacg 840
gaaacacgtta c 851

<210> 26
<211> 263
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> MTB39 (TbH9)

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<400> 26

Val	Ala	Trp	Met	Ser	Val	Thr	Ala	Gly	Gln	Ala	Glu	Leu	Thr	Ala	Ala
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Gln	Val	Arg	Val	Ala	Ala	Ala	Tyr	Glu	Thr	Ala	Tyr	Gly	Leu	Thr	
						20		25				30			
Val	Pro	Pro	Pro	Val	Ile	Ala	Glu	Asn	Arg	Ala	Glu	Leu	Met	Ile	Leu
						35		40			45				
Ile	Ala	Thr	Asn	Leu	Leu	Gly	Gln	Asn	Thr	Pro	Ala	Ile	Ala	Val	Asn
						50		55			60				
Glu	Ala	Glu	Tyr	Gly	Glu	Met	Trp	Ala	Gln	Asp	Ala	Ala	Ala	Met	Phe
						65		70		75			80		
Gly	Tyr	Ala	Ala	Ala	Thr	Ala	Thr	Ala	Thr	Leu	Leu	Pro	Phe		
						85		90			95				
Glu	Glu	Ala	Pro	Glu	Met	Thr	Ser	Ala	Gly	Gly	Leu	Leu	Glu	Gln	Ala
						100		105			110				
Ala	Ala	Val	Glu	Glu	Ala	Ser	Asp	Thr	Ala	Ala	Asn	Gln	Leu	Met	
						115		120			125				
Asn	Asn	Val	Pro	Gln	Ala	Leu	Lys	Gln	Leu	Ala	Gln	Pro	Thr	Gln	Gly
						130		135			140				
Thr	Thr	Pro	Ser	Ser	Lys	Leu	Gly	Gly	Leu	Trp	Lys	Thr	Val	Ser	Pro
						145		150			155			160	
His	Arg	Ser	Pro	Ile	Ser	Asn	Met	Val	Ser	Met	Ala	Asn	Asn	His	Met
						165		170			175				
Ser	Met	Thr	Asn	Ser	Gly	Val	Ser	Met	Thr	Asn	Thr	Leu	Ser	Ser	Met
						180		185			190				
Leu	Lys	Gly	Phe	Ala	Pro	Ala	Ala	Ala	Gln	Ala	Val	Gln	Thr	Ala	
						195		200			205				
Ala	Gln	Asn	Gly	Val	Arg	Ala	Met	Ser	Ser	Leu	Gly	Ser	Ser	Leu	Gly
						210		215			220				
Ser	Ser	Gly	Leu	Gly	Gly	Val	Ala	Ala	Asn	Leu	Gly	Arg	Ala	Ala	
						225		230			235			240	
Ser	Val	Arg	Tyr	Gly	His	Arg	Asp	Gly	Gly	Lys	Tyr	Ala	Xaa	Ser	Gly
						245		250			255				
Arg	Arg	Asn	Gly	Gly	Pro	Ala									
						260									

<210> 27

<211> 474

<212> DNA

<213> Mycobacterium tuberculosis

<220>

<221> CDS

<222> (16)..(450)

<223> alpha-crystalline antigen

<400> 27

attagaggc	atcaa	atg	gcc	acc	acc	ctt	ccc	gtt	cag	cgc	cac	ccg	cg	51
Met	Ala	Thr	Thr	Leu	Pro	Val	Gln	Arg	His	Pro	Arg			
1				5						10				

tcc	ctc	ttc	ccc	gag	ttt	tct	gag	ctg	ttc	gct	ttc	ccg	tca	ttc	99
Ser	Leu	Phe	Pro	Glu	Phe	Ser	Glu	Leu	Phe	Ala	Ala	Phe	Pro	Ser	Phe
15				20							25				

gcc	gga	ctc	cg	ccc	acc	ttc	gac	acc	cg	ttg	atg	cg	ctg	gaa	gac	147
Ala	Gly	Leu	Arg	Pro	Thr	Phe	Asp	Gly	Arg	Leu	Met	Arg	Leu	Glu	Asp	
30					35						40					

gag atg aaa gag ggg cgc tac gag gta cgc gcg gag ctt ccc ggg gtc Glu Met Lys Glu Gly Arg Tyr Glu Val Arg Ala Glu Leu Pro Gly Val	45 50 55 60	195
gac ccc gac aag gac gtc gac att atg gtc cgc gat ggt cag ctg acc Asp Pro Asp Lys Asp Val Asp Ile Met Val Arg Asp Gly Gln Leu Thr	65 70 75	243
atc aag gcc gag cgc acc gag cag aag gac ttc gac ggt cgc tcg gaa Ile Lys Ala Glu Arg Thr Glu Gln Lys Asp Phe Asp Gly Arg Ser Glu	80 85 90	291
tcc gcg tac ggt tcc ttc gtt cgc acg gtg tcg ctg ccg gta ggt gct Phe Ala Tyr Gly Ser Phe Val Arg Thr Val Ser Leu Pro Val Gly Ala	95 100 105	339
gac gag gac gac att aag gcc acc tac gac aag ggc att ctt act gtg Asp Glu Asp Asp Ile Lys Ala Thr Tyr Asp Lys Gly Ile Leu Thr Val	110 115 120	387
tcg gtg gcg gtt tcg gaa ggg aag cca acc gaa aag cac att cag atc Ser Val Ala Val Ser Glu Gly Lys Pro Thr Glu Lys His Ile Gln Ile	125 130 135 140	435
cg ^g tcc acc aac tga ccactgggtc cgtgctgatg accg Arg Ser Thr Asn	145	474

<210> 28
 <211> 144
 <212> PRT
 <213> Mycobacterium tuberculosis

<220>
 <223> alpha-crystalline antigen

<400> 28		
Met Ala Thr Thr Leu Pro Val Gln Arg His Pro Arg Ser Leu Phe Pro		
1 5 10 15		
Glu Phe Ser Glu Leu Phe Ala Ala Phe Pro Ser Phe Ala Gly Leu Arg		
20 25 30		
Pro Thr Phe Asp Thr Arg Leu Met Arg Leu Glu Asp Glu Met Lys Glu		
35 40 45		
Gly Arg Tyr Glu Val Arg Ala Glu Leu Pro Gly Val Asp Pro Asp Lys		
50 55 60		
Asp Val Asp Ile Met Val Arg Asp Gly Gln Leu Thr Ile Lys Ala Glu		
65 70 75 80		
Arg Thr Glu Gln Lys Asp Phe Asp Gly Arg Ser Glu Phe Ala Tyr Gly		
85 90 95		
Ser Phe Val Arg Thr Val Ser Leu Pro Val Gly Ala Asp Glu Asp Asp		
100 105 110		
Ile Lys Ala Thr Tyr Asp Lys Glu Ile Leu Thr Val Ser Val Ala Val		
115 120 125		
Ser Glu Gly Lys Pro Thr Glu Lys His Ile Gln Ile Arg Ser Thr Asn		
130 135 140		

<210> 29
<211> 1211
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<221> CDS
<222> (150)..(1172)
<223> 85 complex antigen (MTB85 complex antigen)

<400> 29
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ttcgaactga gcgtccctcggttgtttcac tcgcccagaa cagattcgac cgcgctgtgc 120
gcagatgaga gttgggattt gtagtagct atg acg ttc ttc gaa cag gtg cga 173
Met Thr Phe Phe Glu Gln Val Arg
1 5
agg ttg cgg agc gca gcg aca acc ctg ccg cgc cgc gtg gct atc gcg 221
Arg Leu Arg Ser Ala Ala Thr Thr Leu Pro Arg Arg Val Ala Ile Ala
10 15 20
gct atg ggg gct gtc ctg gtt tac ggt ctg gtc ggt acc ttc ggc ggg 269
Ala Met Gly Ala Val Leu Val Tyr Gly Leu Val Gly Thr Phe Gly Gly
25 30 35 40
ccg gcc acc gcg ggc gca ttc tct agg ccc ggt ctt cca gtg gaa tat 317
Pro Ala Thr Ala Gly Ala Phe Ser Arg Pro Gly Leu Pro Val Glu Tyr
45 50 55
ctg cag gtg cca tcc gcg tcg atg ggc cgc gac atc aag gtc cag ttc 365
Leu Gln Val Pro Ser Ala Ser Met Gly Arg Asp Ile Lys Val Gln Phe
60 65 70
cag ggc gga ccg cac gcg gtc tac ctg ctc gac ggt ctg cgg gcc 413
Gln Gly Gly Pro His Ala Val Tyr Leu Leu Asp Gly Leu Arg Ala
75 80 85
cag gat gac tac aac ggc tgg gac atc aac acc ccg gcc ttc gag gag 461
Gln Asp Asp Tyr Asn Gly Trp Asp Ile Asn Thr Pro Ala Phe Glu Glu
90 95 100
tac tac cag tca ggg ttg tcg gtg atc atg ccc gtg ggc ggc caa tcc 509
Tyr Tyr Gln Ser Gly Leu Ser Val Ile Met Pro Val Gly Gly Gln Ser
105 110 115 120
agt ttc tac acc gac tgg tat cag ccc tcg cag agc aac ggc cag aac 557
Ser Phe Tyr Thr Asp Trp Tyr Gln Pro Ser Gln Ser Asn Gly Gln Asn
125 130 135
tac acc tac aag tgg gag acc ttc ctt acc aga gag atg ccc gcc tgg 605
Tyr Thr Tyr Lys Trp Glu Thr Phe Leu Thr Arg Glu Met Pro Ala Trp
140 145 150
cta cag gcc aac aag ggc gtg tcc ccg aca ggc aac gcg gcg gtg ggt 653
Leu Gln Ala Asn Lys Gly Val Ser Pro Thr Gly Asn Ala Ala Val Gly
155 160 165

ctt tcg atg tcg ggc ggt tcc gcg ctg atc ctg gcc gcg tac tac ccg Leu Ser Met Ser Gly Gly Ser Ala Leu Ile Leu Ala Ala Tyr Tyr Pro 170 175 180	701
cag cag ttc ccg tac gcc gcg tcg ttg tcg ggc ttc ctc aac ccg tcc Gln Gln Phe Pro Tyr Ala Ala Ser Leu Ser Gly Phe Leu Asn Pro Ser 185 190 195 200	749
gag ggc tgg tgg ccg acg ctg atc ggc ctg gcg atg aac gac tcg ggc Glu Gly Trp Trp Pro Thr Leu Ile Gly Leu Ala Met Asn Asp Ser Gly 205 210 215	797
ggt tac aac gcc aac agc atg tgg ggt ccg tcc agc gac ccg gcc tgg Gly Tyr Asn Ala Asn Ser Met Trp Gly Pro Ser Ser Asp Pro Ala Trp 220 225 230	845
aag cgc aac gac cca atg gtt cag att ccc cgc ctg gtc gcc aac aac Lys Arg Asn Asp Pro Met Val Gln Ile Pro Arg Leu Val Ala Asn Asn 235 240 245	893
acc cgg atc tgg gtg tac tgc ggt aac ggc aca ccc agc gac ctc ggc Thr Arg Ile Trp Val Tyr Cys Gly Asn Gly Thr Pro Ser Asp Leu Gly 250 255 260	941
ggc gac aac ata ccg gcg aag ttc ctg gaa ggc ctc acc ctg cgc acc Gly Asp Asn Ile Pro Ala Lys Phe Leu Glu Gly Leu Thr Leu Arg Thr 265 270 275 280	989
aac cag acc ttc cgg gac acc tac gcg gcc gac ggt gga cgc aac ggg Asn Gln Thr Phe Arg Asp Thr Tyr Ala Ala Asp Gly Gly Arg Asn Gly 285 290 295	1037
gtg ttt aac ttc ccg ccc aac gga aca cac tcg tgg ccc tac tgg aac Val Phe Asn Phe Pro Pro Asn Gly Thr His Ser Trp Pro Tyr Trp Asn 300 305 310	1085
gag cag ctg gtc gcc atg aag gcc gat atc cag cat gtg ctc aac ggc Glu Gln Leu Val Ala Met Lys Ala Asp Ile Gln His Val Leu Asn Gly 315 320 325	1133
gcg aca ccc ccg gcc cct gct gcg ccg gcc gcc tga gccagcaagc Ala Thr Pro Pro Ala Ala Pro Ala Ala Pro Ala Ala 330 335 340	1182
cagcatcggc agcagcgcaa cggccagcgc	1211

<210> 30
<211> 340
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> 85 complex antigen (MTB85 complex antigen)

<400> 30
Met Thr Phe Phe Glu Gln Val Arg Arg Leu Arg Ser Ala Ala Thr Thr
1 5 10 15
Leu Pro Arg Arg Val Ala Ile Ala Ala Met Gly Ala Val Leu Val Tyr
20 25 30

Gly Leu Val Gly Thr Phe Gly Gly Pro Ala Thr Ala Gly Ala Phe Ser
35 40 45
Arg Pro Gly Leu Pro Val Glu Tyr Leu Gln Val Pro Ser Ala Ser Met
50 55 60
Gly Arg Asp Ile Lys Val Gln Phe Gln Gly Gly Pro His Ala Val
65 70 75 80
Tyr Leu Leu Asp Gly Leu Arg Ala Gln Asp Asp Tyr Asn Gly Trp Asp
85 90 95
Ile Asn Thr Pro Ala Phe Glu Glu Tyr Tyr Gln Ser Gly Leu Ser Val
100 105 110
Ile Met Pro Val Gly Gly Gln Ser Ser Phe Tyr Thr Asp Trp Tyr Gln
115 120 125
Pro Ser Gln Ser Asn Gly Gln Asn Tyr Thr Tyr Lys Trp Glu Thr Phe
130 135 140
Leu Thr Arg Glu Met Pro Ala Trp Leu Gln Ala Asn Lys Gly Val Ser
145 150 155 160
Pro Thr Gly Asn Ala Ala Val Gly Leu Ser Met Ser Gly Gly Ser Ala
165 170 175
Leu Ile Leu Ala Ala Tyr Tyr Pro Gln Gln Phe Pro Tyr Ala Ala Ser
180 185 190
Leu Ser Gly Phe Leu Asn Pro Ser Glu Gly Trp Trp Pro Thr Leu Ile
195 200 205
Gly Leu Ala Met Asn Asp Ser Gly Gly Tyr Asn Ala Asn Ser Met Trp
210 215 220
Gly Pro Ser Ser Asp Pro Ala Trp Lys Arg Asn Asp Pro Met Val Gln
225 230 235 240
Ile Pro Arg Leu Val Ala Asn Asn Thr Arg Ile Trp Val Tyr Cys Gly
245 250 255
Asn Gly Thr Pro Ser Asp Leu Gly Gly Asp Asn Ile Pro Ala Lys Phe
260 265 270
Leu Glu Gly Leu Thr Leu Arg Thr Asn Gln Thr Phe Arg Asp Thr Tyr
275 280 285
Ala Ala Asp Gly Gly Arg Asn Gly Val Phe Asn Phe Pro Pro Asn Gly
290 295 300
Thr His Ser Trp Pro Tyr Trp Asn Glu Gln Leu Val Ala Met Lys Ala
305 310 315 320
Asp Ile Gln His Val Leu Asn Gly Ala Thr Pro Pro Ala Ala Pro Ala
325 330 335
Ala Pro Ala Ala
340